



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/880,253
Source: O/PE
Date Processed by STIC: 7/2/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/880,253

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO.X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO.X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

FYI →

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/880,253

DATE: 07/02/2001

TIME: 16:34:08

Input Set : A:\13711.asc

Output Set: N:\CRF3\07022001\I880253.raw

Does Not Comply
Corrected Diskette NeededW-7-
C4-5

3 <110> APPLICANT: The University of Queensland
 4 <120> TITLE OF INVENTION: EXPRESSION MODULATING SEQUENCES
 6 <130> FILE REFERENCE: 2422800/EJH
 8 <140> CURRENT APPLICATION NUMBER: US/09/880,253
 9 <141> CURRENT FILING DATE: 2001-06-13
 11 <150> PRIOR APPLICATION NUMBER: US 60/211,159
 12 <151> PRIOR FILING DATE: 2000-06-13
 14 <160> NUMBER OF SEQ ID NOS: 60
 16 <170> SOFTWARE: PatentIn version 3.0

ERRORED SEQUENCES

71 <210> SEQ ID NO: 6
 72 <211> LENGTH: 8
 73 <212> TYPE: DNA
 74 <213> ORGANISM: synthetic *see item 10 on Error Summary sheet*
 76 <220> FEATURE:
 77 <221> NAME/KEY: misc_feature
 78 <222> LOCATION: (2)..(2)
 79 <223> OTHER INFORMATION: n = any nucleotide
 81 <220> FEATURE:
 82 <221> NAME/KEY: misc_feature
 83 <222> LOCATION: (8)..(8)
 84 <223> OTHER INFORMATION: n = any nucleotide
 86 <400> SEQUENCE: 6

E--> 87 rnccrwgn

88 ⑧

delete at end of file

FyE

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

DATE: 07/02/2001

PATENT APPLICATION: US/09/880,253

TIME: 16:34:09

Input Set : A:\13711.asc

Output Set: N:\CRF3\07022001\I880253.raw

L:4 M:283 W: Missing Blank Line separator, <120> field identifier
L:8 M:270 C: Current Application Number differs, Wrong Format
L:87 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:87 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:8 SEQ:6
L:109 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:664 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59
L:665 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59
L:684 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59
L:687 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59